

ZYU.0603.ST25.txt
SEQUENCE LISTING

<110> Yu, Zailin

Fu, Yan

<120> RECOMBINANT HUMAN ALBUMIN FUSION PROTEINS WITH LONG-LASTING BIOLOGICAL EFFECTS

<130> ZYU-0603

<150> US 06/392,948

<151> 2002-07-01

<160> 40

<170> PatentIn version 3.1

<210> 1

<211> 2229

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA of HSA-hIL-11

<400> 1		
atgaagtggg taacctttat ttcccttctt tttctctta gctcggctta ttccaggggt	60	
gtgttcgtc gagatgcaca caagagttag gttgctcatc ggtttaaaga tttgggagaa	120	
aaaaatttca aagccttgggt gttgattgcc tttgctcagt atcttcagca gtgtccattt	180	
gaagatcatg taaaatttagt gaatgaagta actgaatttgc aaaaaacatg tggctgat	240	
gagtcagctg aaaattgtga caaatcactt catacccttt ttggagacaa attatgcaca	300	
gttgcaactc ttcgtgaaac ctatggtaa atggctgact gctgtgaaa acaagaacct	360	
gagagaaatg aatgcttctt gcaacacaaa gatgacaacc caaacctccc ccgattggtg	420	
agaccagagg ttgatgtgat gtgcactgct tttcatgaca atgaagagac atttttgaaa	480	

ZYU.0603.ST25.txt

aaatacttat atgaaattgc cagaagacat ccttactttt atgccccgga actccttttc	540
tttgctaaaa ggtataaaagc tgctttaca gaatgttgc aagctgctga taaagctgcc	600
tgcctgttgc caaagctcgta tgaacttcgg gatgaaggga aggcttcgtc tgccaaacag	660
agactcaagt gtgccagtc ccaaaaattt ggagaaagag ctttcaaagc atgggcagta	720
gctcgccgtga gccagagatt tcccaaagct gagttgcag aagttccaa gttagtgaca	780
gatcttacca aagtccacac ggaatgctgc catggagatc tgcttgaatg tgctgatgac	840
agggcggacc ttgccaagta tatctgtgaa aatcaagattt cgatctccag taaactgaag	900
gaatgctgtg aaaaacctct gttggaaaaa tcccactgca ttgccaagttt ggaaaatgtat	960
gagatgcctg ctgacttgcc ttcattagct gctgattttt ttgaaagtaa ggatgtttgc	1020
aaaaactatg ctgaggcaaa ggatgtcttc ctggcatgt ttttgtatga atatgcaaga	1080
aggcatcctg attactctgt cgtgctgctg ctgagacttgc ccaagacata tgaaaccact	1140
ctagagaagt gctgtgccgc tgcagatcct catgaatgct atgccaagttt gttcgatgaa	1200
tttaaacctc ttgtgaaaga gcctcagaat ttaatcaaacc aaaaattgtga gcttttttag	1260
cagcttggag agtacaaattt ccagaatgctg ctattagttt gttacaccaa gaaagtaccc	1320
caagtgtcaa ctccaaactct ttagtggatc tcaagaaacc taggaaaagt gggcagcaaa	1380
tgttggaaac atcctgaagc aaaaagaatg ccctgtgcag aagactatct atccgtggtc	1440
ctgaaccagt tatgtgtgtt gcatgagaaa acgcccgtaa gtgacagatg caccatgc	1500
tgcacagaat ctttggtaa caggcgacca tgcttttcag ctctggaaatg cgatgaaaca	1560
tacgttccca aagagtttaa tgctgaaaca ttcaccttcc atgcagatataatgcacactt	1620
tctgagaagg agagacaaat caagaaacaa actgcacttgc ttgagcttgc gaaacacaag	1680
cccaaggcaa caaaagagca actgaaagct gttatggatg atttcgacgc ttttggatg	1740
aagtgtgcacca aggctgacga taaggagacc tgctttggcg aggaggtaa aaaaacttgc	1800
gctgcaagtc aagctgcctt aggcttagct cccatgaccc agacaacgtc cttgaagaca	1860
agctgggtta actgctctaa catgatcgat gaaattataa cacacttaaa gcagccaccc	1920
ttgcctttgc tggacttcaa caacctcaat ggggaagacc aagacattct gatggaaaat	1980
aaccttcgaa ggccaaacctt ggaggcattc aacagggtcg tcaagatgtt acagaacgc	2040
tcagcaatttgc agagcattct taaaaatctc ctgccatgtc tgccctggc cacggccgca	2100
cccacgcgac atccaatcca tatcaaggac ggtgacttgc atgaattccg gaggaaactg	2160
acgttctatc tgaaaaccct tgagaatgctg caggctcaac agacgactttt gagcctcg	2220
atcttttag	2229

zyu.0603.ST25.txt

<211> 763

<212> PRT

<213> Artificial Sequence

<220>

<223> HSA-hIL-11

<400> 2

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
 225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

ZYU.0603.ST25.txt

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Pro Gly Pro Pro Pro Gly Pro
580 585 590

Pro Arg Val Ser Pro Asp Pro Arg Ala Glu Leu Asp Ser Thr Val Leu
595 600 605

Leu Thr Arg Ser Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu
610 615 620

Arg Asp Lys Phe Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro
625 630 635 640

Thr Leu Ala Met Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly
645 650 655

Val Leu Thr Arg Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val
660 665 670

Gln Trp Leu Arg Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro
675 680 685

Glu Leu Gly Thr Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu
690 695 700

ZYU.0603.ST25.txt

Gln Leu Leu Met Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro
705 710 715 720

Pro Ala Pro Pro Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg
725 730 735

Ala Ala His Ala Ile Leu Gly Gly Leu His Leu Thr Leu Asp Trp Ala
740 745 750

Val Arg Gly Leu Leu Leu Lys Thr Arg Leu
755 760

<210> 3

<211> 2229

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA of HSA-hIL-3

<400> 3
atgaagtggg taacctttat ttcccttctt tttctctta gctcggctta ttccagggggt 60
gtgttcgtc gagatgcaca caagagttag gttgctcatc ggttaaaga tttggagaa 120
gaaaatttca aagccttgggt gttgattgcc tttgctcagt atttcagca gtgtccattt 180
gaagatcatg taaaatttagt gaatgaagta actgaatttgc caaaaacatg ttttgctgat 240
gagtcagctg aaaattgtga caaatcactt catacccttt ttggagacaa attatgcaca 300
gttgcactc ttcgtgaaac ctatggtaa atggctgact gctgtgcaaa acaagaacct 360
gagagaaatg aatgcttctt gcaacacaaa gatgacaacc caaacctccc ccgattggtg 420
agaccagagg ttgatgtgat gtgcactgct tttcatgaca atgaagagac atttttgaaa 480
aaatacttat atgaaattgc cagaagacat cttactttt atgccccgga actcctttc 540
tttgctaaaa ggtataaagc tgctttaca gaatgttgcc aagctgctga taaagctgcc 600
tgcctgttgc caaagctcga tgaacttcgg gatgaaggaa aggcttcgtc tgccaaacag 660
agactcaagt gtgccagtct ccaaaaattt ggagaaagag ctttcaaagc atggcagta 720
gctcgctga gccagagatt tcccaaagct gagttgcag aagttccaa gttagtgaca 780
gatcttacca aagtccacac ggaatgctgc catggagatc tgcttgaatg tgctgtgac 840
aggcggacc ttgccaagta tatctgtgaa aatcaagatt cgatctccag taaaactgaag 900

ZYU.0603.ST25.txt

gaatgctgtg	aaaaacctct	gttggaaaaa	tcccactgca	ttgccgaagt	ggaaaatgat	960
gagatgcctg	ctgacttgcc	ttcattagct	gctgattttg	ttgaaagtaa	ggatgtttgc	1020
aaaaactatg	ctgaggcaaa	ggatgtcttc	ctgggcatgt	tttgtatga	atatgcaaga	1080
aggcatcctg	attactctgt	cgtgctgctg	ctgagacttg	ccaagacata	tgaaaccact	1140
ctagagaagt	gctgtccgc	tgcagatcct	catgaatgct	atgccaagt	gttcgatgaa	1200
tttaaacctc	ttgtggaaga	gcctcagaat	ttaatcaaac	aaaattgtga	gcttttgag	1260
cagcttggag	agtacaaatt	ccagaatgcg	ctattagttc	gttacaccaa	gaaagtaccc	1320
caagtgtcaa	ctccaactct	tgttagaggc	tcaagaaacc	tagaaaaagt	gggcagcaa	1380
tgttgtaaac	atcctgaaagc	aaaaagaatg	ccctgtgcag	aagactatct	atccgtggtc	1440
ctgaaccagt	tatgtgttt	gcatgagaaa	acgccagtaa	gtgacagagt	caccaaatgc	1500
tgcacagaat	ccttggtaaa	caggcgacca	tgctttcag	ctctggaagt	cgatgaaaca	1560
tacgttccca	aagagttaa	tgctgaaaca	ttcaccttcc	atgcagatat	atgcacactt	1620
tctgagaagg	agagacaaat	caagaaacaa	actgcacttg	ttgagcttgt	gaaacacaag	1680
cccaaggcaa	caaaagagca	actgaaagct	gttatggatg	atttcgcagc	ttttgttagag	1740
aagtgtgc	aggctgacga	taaggagacc	tgctttgccg	aggaggtaa	aaaacttgtt	1800
gctgcaagtc	aagctgcctt	aggcttagct	cccatgaccc	agacaacgtc	cttgaagaca	1860
agctgggtta	actgctctaa	catgatcgat	gaaattataa	cacactaaa	gcagccacct	1920
ttgccttgc	tggacttcaa	caaccta	ggggaaagacc	aagacattct	gatggaaaat	1980
aacttcgaa	ggccaaacct	ggaggcattc	aacagggctg	tcaagagttt	acagaacgca	2040
tcagcaattg	agagcattct	taaaaatctc	ctgccatgtc	tgccctggc	cacggccgca	2100
cccacgcgac	atccaatcca	tatcaaggac	ggtgactgga	atgaattccg	gaggaaactg	2160
acgttctatc	tgaaaaccct	tgagaatgcg	caggctcaac	agacgacttt	gagcctcgcg	2220
atcttttag						2229

<210> 4

<211> 718

<212> PRT

<213> Artificial Sequence

<220>

<223> HSA-hIL-3

<400> 4

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
 65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
 225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

ZYU.0603.ST25.txt

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Glu Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

ZYU.0603.ST25.txt

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Pro Met Thr Gln Thr Thr
580 585 590

Ser Leu Lys Thr Ser Trp Val Asn Cys Ser Asn Met Ile Asp Glu Ile
595 600 605

Ile Thr His Leu Lys Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn
610 615 620

Leu Asn Gly Glu Asp Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg
625 630 635 640

Pro Asn Leu Glu Ala Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala
645 650 655

Ser Ala Ile Glu Ser Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu
660 665 670

Ala Thr Ala Ala Pro Thr Arg His Pro Ile His Ile Lys Asp Gly Asp
675 680 685

Trp Asn Glu Phe Arg Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu
690 695 700

Asn Ala Gln Ala Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe
705 710 715

<210> 5

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA of HSA-hEPO

<400>	5					
atgaagtggg	taaccttat	ttcccttctt	tttctctta	gctcggtta	ttccaggggt	60
gtgttcgtc	gagatgcaca	caagagttag	gttgctcatc	ggtttaaaga	tttgggagaa	120
gaaaattca	aagccttggt	gttgattgcc	tttgctcagt	atcttcagca	gtgtccattt	180
gaagatcatg	taaaattagt	gaatgaagta	actgaatttgc	caaaaacatg	tgttgctgat	240
gagtcagctg	aaaattgtga	caaattcactt	cataccctt	ttggagacaa	attatgcaca	300
gttgcactc	ttcgtgaaac	ctatggtaaa	atggctgact	gctgtgcaaa	acaagaacct	360
gagagaaatg	aatgcttctt	gcaacacaaa	gatgacaacc	caaaccctccc	ccgattggtg	420
agaccagagg	ttgatgtgat	gtgcactgct	tttcatgaca	atgaagagac	atttttgaaa	480
aaatacttat	atgaaattgc	cagaagacat	ccttactttt	atgccccgga	actccttttc	540
tttgctaaaa	ggtataaagc	tgcttttaca	aatgttgcc	aagctgctga	taaagctgcc	600
tgcctgtgc	caaagctcga	tgaacttcgg	gatgaaggga	aggcttcgtc	tgccaaacag	660
agactcaagt	gtgccagtct	ccaaaaattt	ggagaaagag	ctttcaaagc	atgggcagta	720
gctcgctga	gccagagatt	tcccaaagct	gagtttgcag	aagtttccaa	gttagtgaca	780
gatcttacca	aagtcccacac	ggaatgctgc	catggagatc	tgcttgaatg	tgctgatgac	840
agggcggacc	ttgccaagta	tatctgtgaa	aatcaagatt	cgatctccag	taaactgaag	900
aatgtctgt	aaaaacctct	gttggaaaaaa	tcccactgca	ttgcccgaat	ggaaaatgt	960
gagatgcctg	ctgacttgcc	ttcattagct	gctgattttg	ttgaaaagtaa	ggatgtttgc	1020
aaaaactatg	ctgaggcaaa	ggatgttttc	ctgggcatgt	ttttgtatga	atatgcaaga	1080
aggcatcctg	attactctgt	cgtgctgctg	ctgagacttg	ccaagacata	tgaaaccact	1140
ctagagaagt	gctgtgccgc	tgcagatcct	catgaatgct	atgccaaagt	gttcgatgaa	1200
tttaaacctc	ttgtggaaaga	gcctcagaat	ttaatcaaac	aaaattgtga	gctttttgag	1260
cagcttggag	agtacaaattt	ccagaatgcg	ctattagttc	gttacaccaa	gaaagtaccc	1320
caagtgtcaa	ctccaaactct	tgttagaggc	tcaagaaacc	tagaaaaagt	gggcagcaaa	1380
tgttgtaaac	atcctgaagc	aaaaagaatg	ccctgtgcag	aagactatct	atccgtggtc	1440
ctgaaccagt	tatgtgtgat	gcatgagaaa	acgccagtaa	gtgacagagt	caccaaatgc	1500
tgcacagaat	ccttggtgaa	caggcgacca	tgcttttcag	ctctggaaat	cgatgaaaca	1560
tacgttccca	aagagtttaa	tgctgaaaca	ttcaccttcc	atgcagatat	atgcacactt	1620
tctgagaagg	agagacaaat	caagaaacaa	actgcacttg	ttgagcttgt	gaaacacaag	1680
cccaaggcaa	caaaagagca	actgaaagct	gttatggatg	atttcgcagc	ttttgttagag	1740

ZYU.0603.ST25.txt

aagtgcgtca	aggctgacga	taaggagacc	tgctttcccg	aggagggtaa	aaaacttgtt	1800
gctgcaagtc	aagctgcctt	aggcttaatc	tgtgacagcc	gagtcctgga	gaggtacctc	1860
ttggaggcca	aggaggccga	gaatatcacg	acgggctgtg	ctgaacactg	cagcttgaat	1920
gagaatatca	ctgtcccaga	caccaaagtt	aatttctatg	cctggaagag	gatggaggtc	1980
gggcagcagg	ccgtagaagt	ctggcagggc	ctggccctgc	tgtcggaaagc	tgtcctgcgg	2040
ggccaggccc	tgttggtcaa	ctcttcccag	ccgtgggagc	ccctgcagct	gcatgtggat	2100
aaagccgtca	gtggccttcg	cagcctcacc	actctgcttc	gggctctgcg	agcccagaag	2160
gaagccatct	cccctccaga	tgcggcctca	gctgctccac	tccgaacaat	cactgctgac	2220
actttccgca	aactcttccg	agtctactcc	aatttcctcc	ggggaaagct	gaagctgtac	2280
acaggggagg	cctgcaggac	aggggacaga	tga			2313

<210> 6

<211> 746

<212> PRT

<213> Artificial Sequence

<220>

<223> HSA-hEPO

<400> 6

Asp	Ala	His	Lys	Ser	Glu	Val	Ala	His	Arg	Phe	Lys	Asp	Leu	Gly	Glu
1				5			10							15	

Glu	Asn	Phe	Lys	Ala	Leu	Val	Leu	Ile	Ala	Phe	Ala	Gln	Tyr	Leu	Gln
		20				25						30			

Gln	Cys	Pro	Phe	Glu	Asp	His	Val	Lys	Leu	Val	Asn	Glu	Val	Thr	Glu
		35				40					45				

Phe	Ala	Lys	Thr	Cys	Val	Ala	Asp	Glu	Ser	Ala	Glu	Asn	Cys	Asp	Lys
					50		55			60					

Ser	Leu	His	Thr	Leu	Phe	Gly	Asp	Lys	Leu	Cys	Thr	Val	Ala	Thr	Leu
					65		70		75				80		

Arg	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Asp	Cys	Cys	Ala	Lys	Gln	Glu	Pro
					85			90				95			

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu

100

105

110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Glu Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ile Cys Asp Ser Arg Val Leu
 580 585 590

Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly
 595 600 605

ZYU.0603.ST25.txt

Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr
610 615 620

Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
625 630 635 640

Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg
645 650 655

Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln
660 665 670

Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu
675 680 685

Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala
690 695 700

Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys
705 710 715 720

Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
725 730 735

Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
740 745

<210> 7

<211> 2352

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA of HSA-GCSF

<400> 7
atgaagtggg taaccttat ttcccttctt tttctctta gctcggctta ttccagggtt 60
gtgtttcgtc gagatgcaca caagagttag gttgctcatc ggtttaaaga tttgggagaa 120
gaaaatttca aagccttgggt gttgattgcc tttgctcagt atcttcagca gtgtccattt 180
gaagatcatg taaaatttagt gaatgaagta actgaatttgc caaaaacatg tgttgctgat 240
gagtcagctg aaaattgtga caaatcactt catacccttt ttggagacaa attatgcaca 300
gttgcaactc ttcgtgaaac ctatggtaa atggctgact gctgtgaaa acaagaacct 360

ZYU.0603.ST25.txt

gagagaaaatg aatgcttctt gcaacacaaa gatgacaacc caaacctccc ccgattggtg	420
agaccagagg ttgatgtgat gtgcactgct tttcatgaca atgaagagac atttttgaaa	480
aaatacttat atgaaattgc cagaagacat ccttactttt atgccccgga actcctttc	540
tttgctaaaa ggtataaagc tgctttaca gaatgttgcc aagctgctga taaagctgcc	600
tgccctgtgc caaagctcga tgaacttcgg gatgaaggga aggctcgct tgccaaacag	660
agactcaagt gtgccagttct ccaaaaattt ggagaaagag ctttcaaagc atgggcagta	720
gctcgctga gccagagatt tcccaaagct gagttgcag aagttccaa gttagtgaca	780
gatcttacca aagtccacac ggaatgctgc catggagatc tgcttgaatg tgctgatgac	840
agggcggacc ttgccaagta tatctgtcaa aatcaagatt cgatctccag taaactgaag	900
gaatgctgtg aaaaacctct gttggaaaaa tcccactgca ttgcccgaatg ggaaaatgat	960
gagatgcctg ctgacttgc ttcattagct gctgattttg ttgaaaagtaa ggatgttgc	1020
aaaaactatg ctgaggcaaa ggatgtcttc ctggcatgt ttttgtatga atatgcaaga	1080
aggcatcctg attactctgt cgtgctgctg ctgagacttgc ccaagacata tgaaaccact	1140
ctagagaagt gctgtgccgc tgcaagatct catgaatgct atgccaaagt gttcgatgaa	1200
tttaaacctc ttgtggaaga gcctcagaat ttaatcaaac aaaattgtga gcttttgag	1260
cagcttggag agtacaaatt ccagaatgcg ctattagttc gttacaccaa gaaagtaccc	1320
caagtgtcaa ctccaactct ttagtggatc tcaagaaacc tagaaaaagt gggcagcaaa	1380
tgtttaaac atcctgaagc aaaaagaatg ccctgtgcag aagactatct atccgtggtc	1440
ctgaaccagt tatgtgtgtt gcatgagaaa acgccagtaa gtgacagagt caccaaatgc	1500
tgcacagaat ctttggtaaa cagggcgttca tgcttttcag ctctggaaatg cgatgaaaca	1560
tacgttccca aagagttaa tgctgaaaca ttcaccttcc atgcagatataatgcacactt	1620
tctgagaagg agagacaaat caagaaacaa actgcacitg ttgagcttgt gaaacacaag	1680
cccaaggcaa caaaagagca actgaaagct gttatggatg atttcgagc ttttgttagag	1740
aagtgtgca aggctgacga taaggagacc tgctttggcc aggaggtaa aaaacttgc	1800
gctgcaagtc aagctgcctt aggcttaacc cccctggcc ctggcagctc cctgccccag	1860
agcttccgtc tcaagtgcctt agagcaagtg aggaagatcc agggcgatgg cgccagcgctc	1920
caggagaagc tgggtgcccac ctacaagctg tgccaccccg aggagctggc gctgctcgaa	1980
cactctctgg gcatccccctg ggctccccctg agcagctgcc ccagccaggc cctgcagctg	2040
gcaggctgct tgagccaaact ccatagcgcc ctttccctct accaggggct cctgcaggcc	2100
ctggaaaggga tctcccccca gttgggtccc accttggaca cactgcagct ggacgtcgcc	2160
gactttgcca ccaccatctg gcagcagatg gaagaactgg gaatggcccc tgccctgcag	2220

ZYU.0603.ST25.txt

cccacccagg gtgccatgcc ggccttcgcc tctgcttc acgcggcaggc aggaggggtc 2280
ctagttgcct cccatctgca gagcttcctg gaggtgtcgt accgcgttct acgccacctt 2340
gcccagccct ga 2352

<210> 8

<211> 759

<212> PRT

<213> Artificial Sequence

<220>

<223> HSA-GCSF

<400> 8

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

ZYU.0603.ST25.txt

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

zyu.0603.ST25.txt

Glu Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Thr Pro Leu Gly Pro Ala Ser
580 585 590

Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys
595 600 605

Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr
610 615 620

Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly
625 630 635 640

Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu
645 650 655

Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
660 665 670

ZYU.0603.ST25.txt

Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
675 680 685

Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln
690 695 700

Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly
705 710 715 720

Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
725 730 735

Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val
740 745 750

Leu Arg His Leu Ala Gln Pro
755

<210> 9

<211> 2211

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA of HSA-GMCSF

<400> 9
atgaagtggg taacctttat ttcccttctt tttctctta gctcggtta ttccagggtt 60
gtgttcgtc gagatgcaca caagagttag gttgctcatc ggtttaaaga tttggagaa 120
gaaaatttca aagccttgggt gttgattgcc tttgctcagt atcttcagca gtgtccattt 180
gaagatcatg taaaatttagt gaatgaagta actgaatttg caaaaacatg tggctgtat 240
gagtcagctg aaaattgtga caaatcactt cataccctt ttggagacaa attatgcaca 300
gttgcactc ttctgtgaaac ctatggtaa atggctgact gctgtgaaa acaagaacct 360
gagagaaatg aatgcttctt gcaacacaaa gatgacaacc caaacctccc ccgattggtg 420
agaccagagg ttgatgtgat gtgcactgct tttcatgaca atgaagagac atttttgaaa 480
aaatacttat atgaaattgc cagaagacat cttactttt atgccccgga actcctttc 540
tttgctaaaa ggtataaagc tgctttaca gaatgttgcc aagctgctga taaagctgcc 600
tgccctgttgc caaagctcga tgaacttcgg gatgaaggga aggcttcgtc tgccaaacag 660

ZYU.0603.ST25.txt

agactcaagt	gtgccagtct	ccaaaattt	ggagaaaagag	cttcaaagc	atgggcagta	720
gctcgctga	gccagagatt	tcccaaagct	gagttgcag	aagttccaa	gttagtgaca	780
gatcttacca	aagtccacac	ggaatgctgc	catggagatc	tgcttgaatg	tgctgatgac	840
agggcggacc	ttgccaagta	tatctgtgaa	aatcaagatt	cgatctccag	taaactgaag	900
gaatgctgtg	aaaaacctct	gttggaaaaaa	tcccactgca	ttgcccgaagt	ggaaaatgat	960
gagatgcctg	ctgacttgcc	ttcattagct	gctgattttgc	ttgaaagtaa	ggatgtttgc	1020
aaaaactatg	ctgaggcaaa	ggatgtcttc	ctgggcattgt	ttttgtatga	atatgcaaga	1080
aggcatcctg	attactctgt	cgtgctgctg	ctgagacttg	ccaagacata	tgaaaccact	1140
ctagagaagt	gctgtgccgc	tgcagatcct	catgaatgct	atgccaaagt	gttcgatgaa	1200
tttaaacctc	ttgtggaaga	gcctcagaat	ttaatcaaac	aaaattgtga	gttttttag	1260
cagcttggag	agtacaaatt	ccagaatgcf	ctattagttc	gttacaccaa	gaaagtaccc	1320
caagtgtcaa	ctccaactct	tgttagaggc	tcaagaaacc	tagaaaaagt	gggcagcaaa	1380
tgttgtaaac	atcctgaagc	aaaaagaatg	ccctgtcag	aagactatct	atccgtggc	1440
ctgaaccagt	tatgtgtgtt	gcatgagaaa	acgccagtaa	gtgacagagt	caccaaatgc	1500
tgcacagaat	ccttggtgaa	caggcgacca	tgctttcag	ctctggaaagt	cgtgaaaca	1560
tacgttccca	aagagttaa	tgctgaaaca	ttcacccccc	atgcagatata	atgcacactt	1620
tctgagaagg	agagacaaat	caagaaacaa	actgcacttg	ttgagcttgt	gaaacacaag	1680
cccaaggcaa	caaaagagca	actgaaagct	gttatggatg	atttcgagc	ttttgttag	1740
aagtgtgca	aggctgacga	taaggagacc	tgctttccg	aggaggtaa	aaaacttgtt	1800
gctgcaagtc	aagctgcctt	aggcttagca	ccgcggcgct	cgcggcgccc	cagcacgcag	1860
ccctgggagc	atgtaatgc	catccaggag	gcccgccgct	tcctgaacct	gagtagagac	1920
actgctgctg	agatgaatga	aacagttagaa	gtcatctcag	aatgtttga	cctccaggag	1980
ccgacctgccc	tacagaccccg	cctggagctg	tacaagcagg	gcctgcgggg	cagcctcacc	2040
aagctcaagg	gcccccttgac	catgatggcc	agccactaca	agcagcactg	ccctccaacc	2100
ccggaaactt	cctgtgcaac	ccagattatc	acctttgaaa	gtttcaaaga	gaacctgaaag	2160
gacttctgc	ttgtcatccc	ctttgactgc	tgggagccag	tccaggagtgc	a	2211

<210> 10

<211> 712

<212> PRT

<213> Artificial Sequence

ZYU.0603.ST25.txt

<220>

<223> HSA-GMCSF

<400> 10

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
Page 22

225

230

235

240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Glu Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

ZYU.0603.ST25.txt

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu Ala Pro Ala Arg Ser Pro Ser
580 585 590

Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu Ala Arg
595 600 605

Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr
610 615 620

Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu
625 630 635 640

Gln Thr Arg Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr
645 650 655

Lys Leu Lys Gly Pro Leu Thr Met Met Ala Ser His Tyr Lys Gln His
660 665 670

Cys Pro Pro Thr Pro Glu Thr Ser Cys Ala Thr Gln Ile Ile Thr Phe
675 680 685

Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu Leu Val Ile Pro Phe
690 695 700

Asp Cys Trp Glu Pro Val Gln Glu
705 710

<210> 11

<211> 1830

ZYU.0603.ST25.txt

<212> DNA

<213> Homo sapiens

<400> 11
atgaagtggg taacctttat ttcccttctt tttctctta gctcggtta ttccagggtt 60
gtgttcgtc gagatgcaca caagagttag gttgctcatc ggtttaaaga tttgggagaa 120
gaaaatttca aagccttgggt gttgattgcc tttgctcagt atcttcagca gtgtccattt 180
gaagatcatg taaaatttagt gaatgaagta actgaatttgc caaaaacatg tgttgctgat 240
gagtcagctg aaaattgtga caaatcactt catacccttt ttggagacaa attatgcaca 300
gttgcaactc ttcgtgaaac ctatggtaa atggctgact gctgtgaaa acaagaacct 360
gagagaaatg aatgcttctt gcaacacaaa gatgacaacc caaacctccc ccgattggtg 420
agaccagagg ttgatgtgat gtgcactgct tttcatgaca atgaagagac atttttggaaa 480
aaatacttat atgaaattgc cagaagacat ccttactttt atgccccgga actcctttc 540
tttgctaaaa ggtataaagc tgctttaca gaatgttgc aagctgctga taaagctgcc 600
tgccctgtgc caaagctcga tgaacttcgg gatgaaggaa aggcttcgtc tgccaaacag 660
agactcaagt gtgccagtct caaaaattt ggagaaagag ctttcaaagc atggcagta 720
gctcgctga gccagagatt tcccaaagct gagttgcag aagttccaa gttagtgaca 780
gatcttacca aagtcccacac ggaatgctgc catggagatc tgcttgaatg tgctgatgac 840
agggcggacc ttgccaagta tatctgtgaa aatcaagatt cgatctccag taaaactgaag 900
gaatgctgtg aaaaacctct gttggaaaaa tcccactgca ttgccgaagt ggaaaatgat 960
gagatgcctg ctgacttgcc ttcattagct gctgattttg ttgaaagtaa ggatgtttgc 1020
aaaaactatg ctgaggcaaa ggatgtcttc ctgggcattgt ttttgtatga atatgcaaga 1080
aggcatcctg attactctgt cgtgctgctg ctgagacttgc ccaagacata taaaaccact 1140
ctagagaagt gctgtgccgc tgcaagatcct catgaatgct atgccaagt gttcgatgaa 1200
tttaaacctc ttgtggaaga gcctcagaat ttaatcaaac aaaattgtga gcttttgag 1260
cagcttggag agtacaaatt ccagaatgcg ctattagttc gttacaccaa gaaagtaccc 1320
caagtgtcaa ctccaaactct tgttagaggc tcaagaaacc tagggaaagt gggcagcaaa 1380
tgttgtaaac atccctgaagc aaaaagaatg ccctgtgcag aagactatct atccgtggc 1440
ctgaaccagt tatgtgtgtt gcatgagaaa acgccagtaa gtgacagaggt caccaaatgc 1500
tgcacagaat ccttgggtgaa caggcgacca tgctttcag ctctggaagt ccatgaaaca 1560
tacgttccca aagagttaa tgctgaaaca ttcaccttcc atgcagatat atgcacactt 1620
tctgagaagg agagacaaat caagaaacaa actgcacttgc ttgagcttgc gaaacacaag 1680

ZYU.0603.ST25.txt

cccaaggcaa caaaaagagca actgaaagct gttatggatg atttcgcagc tttttagatg 1740
aagtgcgtca aggctgacga taaggagacc tgcttgcgg aggagggtaa aaaacttgtt 1800
gctgcaagtc aagctgcctt aggcttataa 1830

<210> 12

<211> 609

<212> PRT

<213> Homo sapiens

<400> 12

Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala
20 25 30

His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu
35 40 45

Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
50 55 60

Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
65 70 75 80

Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
85 90 95

Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
100 105 110

Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
115 120 125

His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
130 135 140

Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
145 150 155 160

Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
165 170 175

zyu.0603.ST25.txt

Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
180 185 190

Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
195 200 205

Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys
210 215 220

Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
225 230 235 240

Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
245 250 255

Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
260 265 270

Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
275 280 285

Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
290 295 300

Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
305 310 315 320

Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
325 330 335

Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
340 345 350

Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
355 360 365

Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
370 375 380

Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
385 390 395 400

Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
405 410 415

Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
420 425 430

ZYU.0603.ST25.txt

val Arg Tyr Thr Lys Lys Val Pro Glu Val Ser Thr Pro Thr Leu Val
435 440 445

Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
450 455 460

Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val
465 470 475 480

Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
485 490 495

val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
500 505 510

Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
515 520 525

Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu
530 535 540

Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
545 550 555 560

Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala
565 570 575

Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe
580 585 590

Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly
595 600 605

Leu

<210> 13

<211> 600

<212> DNA

<213> Homo sapiens

<400> 13
atgaactgtg tttgccgcct ggtcctggtc gtgctgagcc tgtggccaga tacagctgtc 60

ZYU.0603.ST25.txt

gcccctggc caccacctgg ccccccctcga	gtttccccag accctcgggc cgagctggac	120
agcaccgtgc tcctgacccg ctctctcctg	gcggacacgc ggcagctggc tgcacagctg	180
agggacaaat tcccagctga cggggaccac	aacctggatt ccctgcccac cctggccatg	240
agtgcggggg cactgggagc tctacagctc	ccaggtgtgc tgacaaggct gcgagcggac	300
ctactgtcct acctgcggca cgtcagtg	ctgcgccccg caggtggctc ttccctgaag	360
accctggagc ccgagctggg caccctgcag	gcccgaactgg accggctgct gcgcggctg	420
cagctcctga tgtcccgcc	ggccctgccc cagccacccc cgacccgccc	480
ctggcgcccc cctcctcagc	ctgggggggc atcagggccg cccacgccc	540
ctgcacactga cacttgactg	ggccgtgagg ggactgctgc tgctgaagac	600

<210> 14

<211> 199

<212> PRT

<213> Homo sapiens

<400> 14

Met Asn Cys Val Cys Arg Leu Val Leu Val Val Leu Ser Leu Trp Pro			
1	5	10	15

Asp Thr Ala Val Ala Pro Gly Pro Pro Gly Pro Pro Arg Val Ser		
20	25	30

Pro Asp Pro Arg Ala Glu Leu Asp Ser Thr Val Leu Leu Thr Arg Ser		
35	40	45

Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu Arg Asp Lys Phe		
50	55	60

Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro Thr Leu Ala Met			
65	70	75	80

Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly Val Leu Thr Arg		
85	90	95

Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val Gln Trp Leu Arg		
100	105	110

Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro Glu Leu Gly Thr		
115	120	125

ZYU.0603.ST25.txt

Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu Gln Leu Leu Met
130 135 140

Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro Pro Ala Pro Pro
145 150 155 160

Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg Ala Ala His Ala
165 170 175

Ile Leu Gly Gly Leu His Leu Thr Leu Asp Trp Ala Val Arg Gly Leu
180 185 190

Leu Leu Leu Lys Thr Arg Leu
195

<210> 15

<211> 582

<212> DNA

<213> Homo sapiens

<400> 15

atgggggtgc acgaatgtcc tgcctggctg tggcttctcc tgtccctgct gtcgctccct 60

ctgggcctcc cagtcctggg cgccccacca cgcctcatct gtgacagccg agtcctggag 120

aggtacctct tggaggccaa ggaggccgag aatatcacga cgggctgtgc tgaacactgc 180

agcttgaatg agaatatcac tgtcccagac accaaagtta atttctatgc ctggaagagg 240

atggaggtcg ggcagcagggc cgtagaagtc tggcagggcc tggccctgct gtcggaagct 300

gtcctgcggg gccaggccct gttggtaac tcttcccagc cgtggagcc cctgcagctg 360

catgtggata aagccgtcag tggcttcgc agcctcacca ctctgttcg ggctctgcga 420

gcccagaagg aagccatctc ccctccagat gcggcctcag ctgctccact ccgaacaatc 480

actgctgaca ctttccgcaa actcttccga gtctactcca atttcctccg gggaaagctg 540

aagctgtaca caggggaggc ctgcaggaca gggacagat ga 582

<210> 16

<211> 193

<212> PRT

<213> Homo sapiens

<400> 16

ZYU.0603.ST25.txt

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Arg

<210> 17

<211> 630

<212> DNA

<213> Homo sapiens

zyu.0603.ST25.txt

<400> 17
ggatccatgg ctggacctgc caccagagc cccatgaagc tggatggccct gcagctgctg 60
ctgtggcaca gtgcactctg gacagtgcag gaagccaccc ccctgggccc tgccagctcc 120
ctgccccaga gcttcctgct caagtgccta gagcaagtga ggaagatcca gggcgatggc 180
gcagcgctcc aggagaagct gtgtgccacc tacaagctgt gccaccccgaa ggagctggtg 240
ctgctcggac actctctggg catccccctgg gctccctgta gcagctgccc cagccaggcc 300
ctgcagctgg caggctgctt gagccaactc catagcgcc ttttcctcta ccaggggctc 360
ctgcaggccc tggaaaggat ctcccccgag ttgggtccca cttggacac actgcagctg 420
gacgtcgccg actttgccac caccatctgg cagcagatgg aagaactggg aatggccct 480
gccctgcagc ccacccaggg tgccatgccc gccttcgcct ctgcttcca gcgcgggca 540
ggaggggtcc tagttgcctc ccacatctgcag agcttcctgg aggtgtcgta ccgcgttcta 600
cgccaccttg cccagccctg agccgaattc 630

<210> 18

<211> 204

<212> PRT

<213> Homo sapiens

<400> 18

Met Ala Gly Pro Ala Thr Gln Ser Pro Met Lys Leu Met Ala Leu Gln
1 5 10 15

Leu Leu Leu Trp His Ser Ala Leu Trp Thr Val Gln Glu Ala Thr Pro
20 25 30

Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu
35 40 45

Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
50 55 60

Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu
65 70 75 80

Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
85 90 95

Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
100 105 110

ZYU.0603.ST25.txt

Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu
115 120 125

Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala
130 135 140

Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
145 150 155 160

Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg
165 170 175

Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
180 185 190

Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
195 200

<210> 19

<211> 448

<212> DNA

<213> Homo sapiens

<400> 19
atgtggctgc agagcctgct gctcttgggc actgtggcct gcagcatctc tgcacccgcc 60
cgctcgccca gccccagcac gcagccctgg gagcatgtga atgccatcca ggaggcccg 120
cgtctcctga acctgagtag agacactgct gctgagatga atgaaacagt agaagtcatc 180
tcagaaatgt ttgacacctca ggagccgacc tgcctacaga cccgcctgga gctgtacaag 240
cagggcctgc ggggcagcct caccaagctc aagggccctt tgaccatgat ggccagccac 300
tacaaggcgc actgcccctcc aaccccgaa acttcctgtg caacccagat tatcaccttt 360
gaaagtttca aagagaacct gaaggacttt ctgcttgtca tcccctttga ctgctgggag 420
ccagtccagg agtgagaccg gccagatg 448

<210> 20

<211> 144

<212> PRT

<213> Homo sapiens

ZYU.0603.ST25.txt

<400> 20

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
 1 5 10 15

Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
 20 25 30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
 35 40 45

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
 50 55 60

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
 65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
 85 90 95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
 100 105 110

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
 115 120 125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
 130 135 140

<210> 21

<211> 459

<212> DNA

<213> Homo sapiens

<400> 21
 atgagccgcc tgcccgccct gctccctgctc caactcctgg tccggcccccgg actccaagct 60
 cccatgaccc agacaacggtc cttgaagaca agctgggtta actgctctaa catgatcgat 120
 gaaattataa cacacttaaa gcagccaccc ttgcctttgc tggacttcaa caacctcaat 180
 ggggaagacc aagacattct gatgaaaaat aacccggaa ggcggaaacct ggaggcattc 240
 aacaggggctg tcaagagttt acagaacgca tcagcaattt agagcattct taaaaatctc 300
 ctgccatgtc tgccctggc cacggccgca cccacgcgac atccaatcca tatcaaggac 360
 ggtgactgga atgaattccg gagggaaactg acgttctatc tgaaaaccct tgagaatgcg 420

<210> 22

<211> 152

<212> PRT

<213> Homo sapiens

<400> 22

Met Ser Arg Leu Pro Val Leu Leu Leu Leu Gln Leu Leu Val Arg Pro
1 5 10 15

Gly Leu Gln Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp
20 25 30

Val Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln
35 40 45

Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln
50 55 60

Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe
65 70 75 80

Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile
85 90 95

Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr
100 105 110

Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg
115 120 125

Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
130 135 140

Thr Thr Leu Ser Leu Ala Ile Phe
145 150

<210> 23

<211> 30

<212> DNA

<213> Artificial Sequence

ZYU.0603.ST25.txt

<220>

<223> Cloning primer

<400> 23

gaattcatga agtgggtaac ctttatttcc

30

<210> 24

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 24

gaattcttat aagcctaagg cagcttgact tgc

33

<210> 25

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 25

catatgaact gtgttgccg cctggtcc

28

<210> 26

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 26

gatatgtatg acacattaa ttccc

25

ZYU.0603.ST25.txt

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 27

ggatccatgg gggtgcacga atgtcc

26

<210> 28

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 28

gaattctcat ctgtccctg tcctgc

26

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 29

ggatccatgg ctggacctgc caccc

25

<210> 30

<211> 26

<212> DNA

<213> Artificial Sequence

ZYU.0603.ST25.txt

<220>

<223> Cloning primer

<400> 30

gaattctcag ggctggcaa ggtggc

26

<210> 31

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 31

ggatccatgt ggctgcagag cctgctgc

28

<210> 32

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 32

gaattctcac tcctggactg gctcc

25

<210> 33

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 33

ctgccttagg cttacctggg ccaccacctg gcc

33

ZYU.0603.ST25.txt

<210> 34
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Cloning primer

<400> 34
tgtcgactca cagccgagtc ttcagcagc 29

<210> 35
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Cloning primer

<400> 35
ctgccttagg cttaatctgt gacagccgag tcc 33

<210> 36
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Cloning primer

<400> 36
cactcgagtc atctgtcccc tgtcctgc 28

<210> 37
<211> 35
<212> DNA
<213> Artificial Sequence

zyu.0603.ST25.txt

<220>

<223> Cloning primer

<400> 37

ctgccttagg cttaaaaaaa ctggggccctg ccagc

35

<210> 38

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 38

ctcgagtcag ggctgggcaa ggtgg

25

<210> 39

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 39

actccttagg ctttagcaccc gccccctcgc ccagc

35

<210> 40

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Cloning primer

<400> 40

ctcgagtcac tcctggactg gctcc

25

ZYU.0603.ST25.txt